

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	7	"1002862".pn.	EPO; DERWENT	OR	OFF	2005/02/01 12:30
L2	2	KIAA near5 prostate	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:31
L3	0	seladin-1 near5 prostate	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:32
L4	3	seladin-1 and prostate	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:33
L5	6	seladin-1	US-PGPUB; USPAT; EPO; DERWENT	OR	OFF	2005/02/01 12:33

Nguyen, D.B., Tang, Y.T., Baughn, M.R., He, A., Thornton, M.,  
Hatala, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,  
Reich, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M.,  
Elliott, V.S., Thangavelu, K., Batra, S. and Ison, C.H.

TITLE  
JOURNAL  
Patent: WO 01096547-A 47 20-DEC-2001;  
Incyte Genomics, Inc. (US)

FEATURES  
Source  
Location/Qualifiers  
1..4772

/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 063497CB1"

## ORIGIN

Query Match 99.6%; Score 398.4; DB 6; Length 4772;  
Best Local Similarity 99.8%; Pred. No. 8e-108;  
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTAAAGAGTGAAGACCTAATACAGCGGATGCTACAGAGATCCCAAGAGAGGC 60  
Db 910 GCTTAAAGAGTGAAGACCTAATACAGCGGATGCTACAGAGATCCCAAGAGAGGC 969  
Qy 61 TTTCTTAAAGAGATGTAATATCATCTTGGCTTCAAGGAGTGAACCTTCAACAGCTAC 120  
Db 970 TTTCTTAAAGAGATGTAATATCATCTTGGCTTCAAGGAGTGAACCTTCAACAGCTAC 1029  
Qy 121 AAAGATTAACATTCCTCCCTTGTGTCTATACAAAATCTTCGGAAGAGAGCAACAGCAT 180  
Db 1030 AAAGATTAACATTCCTCCCTTGTGTCTATACAAAATCTTCGGAAGAGAGCAACAGCAT 1089  
Qy 181 CATTACAGCGCATGTGCTTGGGACATACAGCGGATGAGACCGCATTTGTAAGAGCCCTGGA 240  
Db 1090 CATTACAGCGCATGTGCTTGGGACATACAGCGGATGAGACCGCATTTGTAAGAGCCCTGGA 1149  
Qy 241 AACCAACAGTATTAACATATCACAGCCCACTCTTCTGCTGTAAGAGATCTGAG 300  
Db 1150 AACCAACAGTATTAACATATCACAGCCCACTCTTCTGCTGTAAGAGATCTGAG 1209  
Qy 301 AGAAAGCAAGAGAAAGAAATACAGACGATCTGCAAGCCCGAGCAATATCAAGGCCCA 360  
Db 1210 AGAAAGCAAGAGAAAGAAATACAGACGATCTGCAAGCCCGAGCAATATCAAGGCCCA 1269  
Qy 361 GTTAGGCGATGATGCGCAACCAAAATGATGATACCCCGAG 400  
Db 1270 GTTAGGCGATGATGCGCAACCAAAATGATGATACCCCGAG 1309

RESULT 5  
HUNKIAQ 4882 bp mRNA linear PRI 10-MAY-2002  
LOCUS Human mRNA for KIAA0096 gene, partial cds.  
DEFINITION D43636  
VERSION D43636.2 GI:20521877  
KEYWORDS KIAA0096.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
1 Nagase, T., Miyajima, N., Tanaka, A., Sazuka, T., Seki, N., Sato, S.,  
Tabata, S., Ishikawa, K.-i., Kawarabayashi, Y., Kotani, H. and Nomura, N.  
Prediction of the coding sequences of unidentified human genes.  
III. The coding sequences of 40 new genes (KIAA0081-KIAA0120)  
deduced by analysis of cDNA clones from human cell line KG-1

JOURNAL  
MEDLINE  
PUBMED  
95308323  
7788527

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 4882)  
Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.  
Direct Submission  
Submitted (24-NOV-1994) Otsu Ohara, Kazusa DNA Research Institute;  
1532-3, Yana, Kistazazu, Chiba 292-0812, Japan

COMMENT  
FEATURES  
Source  
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)  
On May 9, 2002 this sequence version replaced gi:598957.  
Location/Qualifiers  
1..4882

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="ha0124081"  
/sex="male"  
/cell\_line="KG-1"  
/cell\_type="myeloblast"  
/tissue\_type="brain"  
/clone\_lib="pbluescript SK plus"  
/note="This sequence was obtained by subcloning of the DNA  
fragments derived from two cDNA clones (1 - 1013 was  
derived from a RT-PCR product (lung) and 1014 - 4882 was  
derived from ha01240)."  
1..4882  
/gene="KIAA0096"  
/gene="KIAA0096"  
/note="KIAA0096 gene product is related to a protein  
kinase."  
/codon\_start=2  
/protein\_id="BA07744.2"  
/db\_xref="GI:20521878"

/trna1action="SMAGPRGIDGKIAGLYDUDKTLGRGFAPVVKLARIHFTGEKVA  
VKVLDKTLATLGLFOEVRCKLVQHNIVRLKLEVIDTOKLLELGGGMF  
DYIMKEBGLNEDLAKYPAQIVAHISYCHKLAVHVRDKEPVVFEKQGLYKDF  
GFENKPOPKKLTTCGSLAAYSPAILLDEVDPAVDVLSGLVITLPHLVGGPPDE  
ANDSELTHIMDKTTPVSHVKECDLITRMQRPKRSASLEIENHFWLQGVPS  
PARKYPLVSYNLSBEBNSIIQMVLDADRAIVALELNTNHNITATYFLA  
ERLRKQKEIOTRSAPSNIAQFROSPKTIIVPOLEDLDTATPSHATVPS  
ARAADSVLGNHRSKGLCDASAKODLPGLAGPALSTVPASLKEPTAGSGKCLPVEDE  
EEDDEPKMPSLSTOVLRKPSVTRLSRKAPLYNOIFEEGSDDEPDMENLP  
KLSRLKMTLASPTVHKYHRRKSGORSSCSSSEFSDDSERRRLDQSGTYSKH  
RRSSGPRGSEBDEGQSPNSAGVDKASENNAGGSSSSGSGAPNTSGT  
RCAGPSNMQLSRSRAGSLVSLKMSLCLSGQLHSGTKYIIPONGISFSSVKQ  
KSTWKNICISTGNAGQVPAVGGIKFSDHMDADTTLEERI KSNLKNVYLQPLCEKT  
ISVNIORNPKEGILCASPSASCCHVI"

## ORIGIN

Query Match 99.6%; Score 398.4; DB 9; Length 4882;  
Best Local Similarity 99.8%; Pred. No. 8e-108;  
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTAAAGAGTGAAGACCTAATACAGCGGATGCTACAGAGATCCCAAGAGAGGC 60  
Db 718 GCTTAAAGAGTGAAGACCTAATACAGCGGATGCTACAGAGATCCCAAGAGAGGC 777  
Qy 61 TTTCTTAAAGAGATGTAATATCATCTTGGCTTCAAGGAGTGAACCTTCAACAGCTAC 120  
Db 778 TTTCTTAAAGAGATGTAATATCATCTTGGCTTCAAGGAGTGAACCTTCAACAGCTAC 837  
Qy 121 AAAGATTAACATTCCTCCCTTGTGTCTATACAAAATCTTCGGAAGAGAGCAACAGCAT 180  
Db 838 AAAGATTAACATTCCTCCCTTGTGTCTATACAAAATCTTCGGAAGAGAGCAACAGCAT 897  
Qy 181 CATTACAGCGCATGTGCTTGGGACATACAGCGGATGAGACCGCATTTGTAAGAGCCCTGGA 240  
Db 898 CATTACAGCGCATGTGCTTGGGACATACAGCGGATGAGACCGCATTTGTAAGAGCCCTGGA 957  
Qy 241 AACCAACAGTATTAACATATCACAGCCCACTCTTCTGCTGTAAGAGATCTGAG 300  
Db 958 AACCAACAGTATTAACATATCACAGCCCACTCTTCTGCTGTAAGAGATCTGAG 1017  
Qy 301 AGAAAGCAAGAGAAAGAAATACAGACGATCTGCAAGCCCGAGCAATATCAAGGCCCA 360  
Db 1018 AGAAAGCAAGAGAAAGAAATACAGACGATCTGCAAGCCCGAGCAATATCAAGGCCCA 1077  
Qy 361 GTTAGGCGATGATGCGCAACCAAAATGATGATACCCCGAG 400  
Db 1078 GTTAGGCGATGATGCGCAACCAAAATGATGATACCCCGAG 1117

Qy		61	GAAGAACAGCTGTATTTTTCGTAATGTGTGATAATATATATATTAAATTAATGACTCTTGCC	120
Db		3860	GAAAAACAGCTCTTGATTTTTTCGTAATGTGTGATAATATATATATTAAATTAATGACTCTTGCC	3915
Qy		121	AATTCATCTGATATTTAAGATGTGCACATCTTGAACCAATTTTAAAGATGCTGTAG	180
Db		3920	AATTCATCTGATATTTAAGATGTGCACATCTTGAACCAATTTTAAAGATGCTGTAG	3975
Qy		181	ACCGAATTAAAGATAATCCCTACCAAATGAAAATTGATGTGTAAAGGGGTACAGAAT	240
Db		3980	ACCGAATTAAAGATAATCCCTACCAAATGAAAATTGATGTGTAAAGGGGTACAGAAT	4035
Qy		241	TATCAACTGATTTGGCAGTTGCTGCCATGCTGTGTTATTTCCCATTTGTGTAACAAT	300
Db		4040	TATCAACTGATTTGGCAGTTGCTGCCATGCTGTGTTATTTCCCATTTGTGTAACAAT	4095
Qy		301	TGACACGATGTGACAAATGGGAAAAAAAAATCCAATATAAAGACATATTTGGTGTTC	360
Db		4100	TGACACGATGTGACAAATGGGAAAAAAAAATCCAATATAAAGACATATTTGGTGTTC	4155
Qy		361	AGCAAT 366	
Db		4160	AGCAAT 4165	
RESULT 4				
HOMKIAAO				
LOCUS	HUMKIAAO	4882 bp	mRNA	linear
DEFINITION	Human mRNA for KIAA0096 gene, partial cds.			PRI 10-MAY-2002
ACCESSION	D43636			
VERSION	D43636.2	GI:20521877		
KEYWORDS	KIAA0096.			
SOURCE	Homio sapiens (human)			
ORGANISM	Homio sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE				
AUTHORS	Nagase,T., Miyajima,N., Tanaka,A., Sazuka,T., Seki,I., Sato,S.,			
TITLE	Tabata,S., Ishikawa,K.-I., Kawarabayashi,Y., Koriama,H. and Nomura,N.			
	Prediction of the coding sequences of unidentified human genes.			
	III. The coding regions of 40 new genes (KIAA0081-KIAA0120)			
	deduced by analysis of cDNA clones from human cell line KG-1			
JOURNAL	DNA Res 2 (1993) 37-43 (1995)			
MEDLINE	95308325			
PUBMED	7788527			
REFERENCE	2 (bases 1 to 4882)			
AUTHORS	Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-NOV-1994) Oasamu Ohara, Kazusa DNA Research Institute;			
	1532-3 J. Yana, Kisarazu, Chiba 292-0812, Japan			
	(E-mail:cdna1nk@kazusa.or.jp, Tel:+81-438-52-3913)			
COMMENT	On May 9, 2002 this sequence version replaced gi:59857.			
FEATURES	Location/Qualifiers			
Source	1..4882			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="ha0124081"			
	/sex="male"			
	/cell_line="KG-1"			
	/cell_type="myeloblast"			
	/tissue_type="brain"			
	/clone_id="pb1uescriptII SK plus"			
	/note="This sequence was obtained by subcloning of the DNA			
	fragments derived from two cDNA clones (1 - 1013 was			
	derived from a RT-PCR product (lung) and 1014 - 4882 was			
	1..4882			
	/gene="KIAA0096"			
	<1..2302			
	/gene="KIAA0096"			
	/note="KIAA0096 gene product is related to a protein			
	kinese."			
CDS				
gene				

Query Match	100.0%	Score 366	DB 9	Length 4882
Best Local Similarity	100.0%	Pred. No. 1,4e-64		
Matches 366	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Db	1	CCCTTAACCTGCTCTCAAAAGTTCATTAAGTTCACAGAGTGTATTAATTAATTTGTCG	60	
QY	4517	CCCTTAACCTGCTCTCAAAAGTTCATTAAGTTCACAGAGTGTATTAATTAATTTGTCG	4576	
Db	61	GAAGAAACAGTCTGTATTTTCTGTATGCTGTATTAATTAATTAATTAATTTGTCG	120	
QY	4577	GAAGAAACAGTCTGTATTTTCTGTATGCTGTATTAATTAATTAATTAATTTGTCG	4633	
Db	121	AATTCATCTGTATTTAAAGTGTGACATCTTGACACCAATTTTAAAGATAGCTGTAG	180	
QY	4637	AATTCATCTGTATTTAAAGTGTGACATCTTGACACCAATTTTAAAGATAGCTGTAG	4696	
Db	181	ACCGAATTAAGATTAATCCCTACCAAGGAAATTAAGTGTGTGTTAAGAGGTACAGAT	240	
QY	4657	ACCGAATTAAGATTAATCCCTACCAAGGAAATTAAGTGTGTGTTAAGAGGTACAGAT	4756	
Db	241	TATCACTGATTTGTCAGTGTGCTTCCCAATCTGTTGATTTCCCTCATTTGTGTAACAT	300	
QY	4757	TATCACTGATTTGTCAGTGTGCTTCCCAATCTGTTGATTTCCCTCATTTGTGTAACAT	4816	
Db	301	TGACAGGTATGTGCAAAATGGGAAAAATCCAAATTAATTAAGTGAATATTTGCTTC	360	
QY	4817	TGACAGGTATGTGCAAAATGGGAAAAATCCAAATTAATTAAGTGAATATTTGCTTC	4876	
Db	361	AGCAAT 366		
QY	4877	AGCAAT 4882		

RESULT 5

BC071567

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

5140 bp

mRNA

linear

PRI 25-JUN-2004

Homo sapiens SNF-1 related kinase, mRNA (cDNA clone MGC:87067

IMAGE:4375623), complete cds.

BC071567

BC071567.1 GI:47939483

MGC.

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 5140)

Straussberg, R. L., Feingold, E. A., Grouse, L. H., Dege, J. G.,

Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altshul, S. F., Zeeberg, B., Bueltow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heile, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Scapleton, M., Soares, M. B., Bonaldi, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M. J., Uedini, T. B., Toshiyuki, S.,

Carninci, P., Pflanze, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.  
Gene expression profiles in liver cancer  
Patent: WO 0229103-A 1609 11-APR-2002;  
JOURNAL GENE LOGIC INC (US)

FEATURES  
source  
1. .4187  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="EMBL/GenBank Accession No. D13643"

ORIGIN

Query Match 100.0%; Score 400; DB 6; Length 4187;  
Best Local Similarity 100.0%; Pred. No. 1.8e-67;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCAACCCGAGGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60  
DB 1 GGGCGCAACCCGAGGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60  
QY 61 CCGGTGCGCGCT 120  
DB 61 CCGGTGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
DB 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
QY 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
DB 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
QY 181 TCTACTACTAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
DB 181 TCTACTACTAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
QY 241 AGCAGCGCGTGGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
DB 241 AGCAGCGCGTGGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 301 CCTTATGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
DB 301 CCTTATGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
QY 361 AGAGACACACAAAACATCATGATCACTGATGAGCAT 400  
DB 361 AGAGACACACAAAACATCATGATCACTGATGAGCAT 400

RESULT 7  
AX828407 4187 bp DNA linear PAT 12-DEC-2003  
LOCUS Sequence 53 from Patent WO03074073.  
ACCESSION AX828407  
VERSION AX828407.1 GI:39838407  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
Al-Mahmoud, S., Colin, S. and Schneider, C.  
Genes involved in regulating angiogenesis, pharmaceutical  
preparations containing same and applications thereof  
Patent: WO 03074073-A 53 12-SEP-2003;  
JOURNAL Gene Signal (FR)

FEATURES  
source  
1. .4187  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 400; DB 6; Length 4187;  
Best Local Similarity 100.0%; Pred. No. 1.8e-67;  
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCGCAACCCGAGGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60  
DB 1 GGGCGCAACCCGAGGCTTACCGCGCGCGCGCAACATGAGCCCGCGTGCCTG 60  
QY 61 CCGGTGCGCGCT 120  
DB 61 CCGGTGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120  
QY 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
DB 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
QY 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
DB 121 TCACACGAGCGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 180  
QY 181 TCTACTACTAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
DB 181 TCTACTACTAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
QY 241 AGCAGCGCGTGGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
DB 241 AGCAGCGCGTGGGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 301 CCTTATGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
DB 301 CCTTATGTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
QY 361 AGAGACACACAAAACATCATGATCACTGATGAGCAT 400  
DB 361 AGAGACACACAAAACATCATGATCACTGATGAGCAT 400

RESULT 8  
HUMSC390 4187 bp mRNA linear PRI 06-OCT-2001  
LOCUS Homo sapiens mRNA for KIAA0018 protein, partial cds.  
DEFINITION D13643  
ACCESSION D13643.2 GI:6630631  
VERSION D13643.2  
KEYWORDS KIAA0018 protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y.,  
Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.  
Prediction of the coding sequences of unidentified human genes. I.  
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
analysis of randomly sampled cDNA clones from human immature  
myeloid cell line KG-1  
myeloid cell line KG-1 (supplement)  
DNA Res. 1 (1), 47-56 (1994)  
JOURNAL 96051187  
MEDLINE 7584026  
PUBMED

REFERENCE 2  
Nomura, N., Miyajima, N., Sazuka, T., Tanaka, A., Kawarabayashi, Y.,  
Sato, S., Nagase, T., Seki, N., Ishikawa, K. and Tabata, S.  
Prediction of the coding sequences of unidentified human genes. I.  
The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
analysis of randomly sampled cDNA clones from human immature  
myeloid cell line KG-1 (supplement)  
DNA Res. 1 (1), 47-56 (1994)  
JOURNAL 96051187  
MEDLINE 7584028  
PUBMED

REFERENCE 3  
(bases 1 to 4187)  
Ohara, O., Nagase, T., Kikuno, R. and Nomura, N.  
Direct Submission  
Submitted (11-NOV-1992) Osamu Ohara, Kazusa DNA Research Institute;  
1532-3, Yata, Kisarazu, Chiba 292-0812, Japan  
(E-mail: cdnainfo@kazusa.or.jp, Tel: +81-438-52-3913)  
On Dec 22, 1999 this sequence version replaced gi:265996.  
Sequence updated (20-Dec-1999).  
Location/Qualifiers

COMMENT

FEATURES



Gene	1. .4187
CDS	/gene="X1AA0018" <1. .1589

Altschuld, S.F., Zeeberg, B., Buecaw, K., Schneider, C., Shao, N., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,